

Patent Application US/07/807,043B



(1) GENERAL INFORMATION:

- (i) APPLICANTS: Boon, Thierry, Van den Eynde, Beno t
- (ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor Rejection Antigens and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Felfe & Lynch
 - (B) STREET: 805 Third Avenue
 - (C) CITY: New York City
 - (D) STATE: New York
 - (F) ZIP: 10022
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 - (B) COMPUTER: IBM
 - (C) OPERATING SYSTEM: PC-DOS
 - (D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 07/807,043
 - (B) FILING DATE: 12-DECEMBER-1991
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 07/764,364
 - (B) FILING DATE: 23-SEPTEMBER-1991
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 07/728,838
 - (B) FILING DATE: 9-JULY-1991
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 07/705,702
 - (B) FILING DATE: 23-May-1991
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Hanson, Norman D.
 - (B) REGISTRATION NUMBER: 30,946
 - (C) REFERENCE/DOCKET NUMBER: LUD 253.3
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (212) 688-9200
 - (B) TELEFAX: (212) 838-3884

(2) INFORMATION FOR SEQUENCE ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid

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54 (C) STRANDEDNESS: singular
55 (D) TOPOLOGY: linear
56 (ii) MOLECULE TYPE: genomic DNA
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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62 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG 60
63 ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT 120
64 CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTCGA AGTTCCGCCT ACAGCTCTAG 180
65 CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCCTC 240
66 CCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
67 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG CATGCATTGT 360
68 GTCAACGCCA TTGACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT 420
69 TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTGTG CC 462
70
71
72 (2) INFORMATION FOR SEQUENCE ID NO: 2:
73 (i) SEQUENCE CHARACTERISTICS:
74 (A) LENGTH: 675 base pairs
75 (B) TYPE: nucleic acid
76 (C) STRANDEDNESS: singular
77 (D) TOPOLOGY: linear
78 (ii) MOLECULE TYPE: genomic DNA
79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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81
82 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT 48
83 Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
84 5 10 15
85
86 GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA 96
87 Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
88 20 25 30
89
90 GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA 144
91 Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
92 35 40 45
93
94 AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG 192
95 Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
96 50 55 60
97
98 TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC 240
99 Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
100 65 70 75 80
101
102 TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC 288
103 Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
104 85 90 95
105
106 GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 336

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107 Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
108 100 105 110
109
110 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG 384
111 Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
112 115 120 125
113
114 GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG 432
115 Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
116 130 135 140
117
118 GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG 480
119 Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
120 145 150 155 160
121
122 AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC 528
123 Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
124 165 170 175
125
126 CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT 576
127 Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
128 180 185 190
129
130 GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG 624
131 Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
132 195 200 205
133
134 GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 672
135 Glu Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
136 210 215 220 225
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138 TAG 675
139
140 (2) INFORMATION FOR SEQUENCE ID NO: 3:
141 (i) SEQUENCE CHARACTERISTICS:
142 (A) LENGTH: 228 base pairs
143 (B) TYPE: nucleic acid
144 (C) STRANDEDNESS: singular
145 (D) TOPOLOGY: linear
146 (ii) MOLECULE TYPE: genomic DNA
147 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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150
151
152 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT 60
153 TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT 120
154 TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACCTT CATATGATAC 180
155 ATAGGATTAC ACTTGACCT GTTAAAAATA AAAGTTTGAC TTGCATAC 228
156
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159 (2) INFORMATION FOR SEQUENCE ID NO: 4:

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160 (i) SEQUENCE CHARACTERISTICS:
161 (A) LENGTH: 1365 base pairs
162 (B) TYPE: nucleic acid
163 (C) STRANDEDNESS: singular
164 (D) TOPOLOGY: linear
165 (ii) MOLECULE TYPE: genomic DNA
166 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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169
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171 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50
172 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT 100
173 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150
174 AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT 200
175 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
176 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
177 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG 350
178 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400
179 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450
180 ACCCTTTGTG CC 462
181 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
182 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
183 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
184 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
185 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
186 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
187 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756
188 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
189 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840
190 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
191 GCT GAG GAA ATG GGT GCT GGT AAC TGT GCC TGT GTT CCT 924
192 GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT 966
193 TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG 1008
194 AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT 1050
195 GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG 1092
196 GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 1134
197 TAG 1137
198 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG 1187
199 TTGTTTTTTT TTCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA 1237
200 ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT 1287
201 CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT 1337
202 GTTAAAAATA AAAGTTTGAC TTGCATAC 1365
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204
205
206 (2) INFORMATION FOR SEQUENCE ID NO: 5:
207 (i) SEQUENCE CHARACTERISTICS:
208 (A) LENGTH: 4698 base pairs
209 (B) TYPE: nucleic acid
210 (C) STRANDEDNESS: singular
211 (D) TOPOLOGY: linear
212 (ii) MOLECULE TYPE: genomic DNA

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213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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219	CAGCCAATGA	GCTTACTGTT	CTCGTGGGGG	GTTTGTGAGC	CTTGGGTAGG	150
220	AAGTTTTGCA	AGTTCCGCCT	ACAGCTCTAG	CTTGTGAATT	TGTACCCTTT	200
221	CACGTAAAAA	AGTAGTCCAG	AGTTTACTAC	ACCCTCCCTC	CCCCCTCCCA	250
222	CCTCGTGCTG	TGCTGAGTTT	AGAAGTCTTC	CTTATAGAAG	TCTTCCGTAT	300
223	AGAACTCTTC	CGGAGGAAGG	AGGGAGGACC	CCCCCCTTTT	GCTCTCCCAG	350
224	CATGCATTGT	GTCAACGCCA	TTGCACTGAG	CTGGTCGAAG	AAGTAAGCCG	400
225	CTAGCTTGCG	ACTCTACTCT	TATCTTAACT	TAGCTCGGCT	TCCTGCTGGT	450
226	ACCCTTTGTG	CC				462
227	ATG TCT GAT	AAC AAG AAA	CCA GAC AAA	GCC CAC AGT	GGC TCA	504
228	GGT GGT GAC	GGT GAT GGG	AAT AGG TGC	AAT TTA TTG	CAC CGG	546
229	TAC TCC CTG	GAA GAA ATT	CTG CCT TAT	CTA GGG TGG	CTG GTC	588
230	TTC GCT GTT	GTC ACA AGT	TTT CTG GCG	CTC CAG	ATG TTC	630
231	ATA GAC GCC	CTT TAT GAG	GAG CAG TAT	GAA AGG GAT	GTG GCC	672
232	TGG ATA GCC	AGG CAA AGC	AAG CGC ATG	TCC TCT GTC	GAT GAG	714
233	GAT GAA GAC	GAT GAG GAT	GAT GAG GAT	GAC TAC TAC	GAC GAC	756
234	GAG GAC GAC	GAC GAC GAT	GCC TTC TAT	GAT GAT GAG	GAT GAT	798
235	GAG GAA GAA	GAA TTG GAG	AAC CTG ATG	GAT GAT GAA	TCA GAA	840
236	GAT GAG GCC	GAA GAA GAG	ATG AGC GTG	GAA ATG GGT	GCC GGA	882
237	GCT GAG GAA	ATG GGT GCT	GGC GCT AAC	TGT GCC T		916
238	GTGAGTAACC	CGTGGTCTTT	ACTCTAGATT	CAGGTGGGGT	GCATTCTTTA	966
239	CTCTTGCCCA	CATCTGTAGT	AAAGACCACA	TTTTGGTTGG	GGGTCATTGC	1016
240	TGGAGCCATT	CCTGGCTCTC	CTGTCCACGC	CTATCCCCGC	TCCTCCCATC	1066
241	CCCCACTCCT	TGCTCCGCTC	TCTTTCTTTT	TCCCACCTTG	CCTCTGGAGC	1116
242	TTCAGTCCAT	CCTGCTCTGC	TCCCTTTCCC	CTTGCTCTC	CTTGCTCCCC	1166
243	TCCCCCTCGG	CTCAACTTTT	CGTGCCTTCT	GCTCTCTGAT	CCCCACCCTC	1216
244	TTCAGGCTTC	CCCATTGTCT	CCTCTCCCGA	AACCCCTCCC	TTCTGTCTCC	1266
245	CCTTTTCGCG	CCTTTTCTTT	CCTGCTCCCC	TCCCCCTCCC	TATTTACCTT	1316
246	TCACCAGCTT	TGCTCTCCCT	GCTCCCCCTC	CCCTTTTGCA	CCTTTTCTTT	1366
247	TCCTGCTCCC	CTCCCCCTCC	CCTCCCTGTT	TACCCTTCAC	CGCTTTTCTT	1416
248	CTACCTGCTT	CCCTCCCCCT	TGCTGCTCCC	TCCCTATTTG	CATTTTCGGG	1466
249	TGCTCCTCCC	TCCCCCTCCC	CCTCCCTCCC	TATTTGCATT	TTCGGGTGCT	1516
250	CCTCCCTCCC	CCTCCCCAGG	CCTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	1566
251	TTGGTTTTTC	GAGACAGGGT	TTCTCTTTGT	ATCCCTGGCT	GTCTGGCAC	1616
252	TCACTCTGTA	GACCAGGCTG	GCCTCAAAC	CAGAAATCTG	CCTGCCTCTG	1666
253	CCTCCCAAAT	GCTGGGATTA	AAGGCTTGCA	CCAGGACTGC	CCCAGTGCAG	1716
254	GCCTTTCTTT	TTTCTCCTCT	CTGGTCTCCC	TAATCCCTTT	TCTGCATGTT	1766
255	AACTCCCCTT	TTGGCACCTT	TCCTTTACAG	GACCCCTCC	CCCTCCCTGT	1816
256	TTCCCTTCCG	GCACCCTTCC	TAGCCCTGCT	CTGTTCCCTC	TCCCTGCTCC	1866
257	CCTCCCCCTC	TTTGCTCGAC	TTTTCAGCAG	CTTACCTCTC	CCTGCTTTCT	1916
258	GCCCCGTTCC	CCTTTTTTGT	GCCTTTCCTC	CTGGCTCCCC	TCCACCTTCC	1966
259	AGCTCACCTT	TTTGTTTGT	TGGTTGTTG	GTTGTTGGT	TTGCTTTTTT	2016
260	TTTTTTTTTT	GCACCTTGTT	TTCCAAGATC	CCCCCTCCCC	TCCGGCTTCC	2066
261	CCTCTGTGTG	CCTTTCTCTG	TCCCTCCCCC	TCGCTGGCTC	CCCCTCCCTT	2116
262	TCTGCCTTTC	CTGTCCCTGC	TCCCTTCTCT	GCTAACCTTT	TAATGCCTTT	2166
263	CTTTTCTAGA	CTCCCCCTCC	CAGGCTTGCT	GTTTGCTTCT	GTGCACTTTT	2216
264	CCTGACCCTG	CTCCCCCTCC	CCTCCAGCT	CCCCCTCTT	TTCCACCTC	2266
265	CCTTTCTCCA	GCCTGTCACC	CCTCCTTCTC	TCCTCTCTGT	TTCTCCCACT	2316

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266	TCCTGCTTCC	TTTACCCCTT	CCCTCTCCCT	ACTCTCCTCC	CTGCCTGCTG	2366
267	GACTTCCTCT	CCAGCCGCCC	AGTTCCCTGC	AGTCCTGGAG	TCTTTCCTGC	2416
268	CTCTCTGTCC	ATCACTTCCC	CCTAGTTTCA	CTTCCCTTTC	ACTCTCCCTT	2466
269	ATGTGTCTCT	CTTCCTATCT	ATCCCTTCCT	TTCTGTCCCC	TCTCCTCTGT	2516
270	CCATCACCTC	TCTCCTCCCT	TCCCTTTTCT	CTCTCTTCCA	TTTTCTTCCA	2566
271	CCTGCTTCTT	TACCCTGCCT	CTCCCATTGC	CCTCTTACCT	TTATGCCCAT	2616
272	TCCATGTCCC	CTCTCAATTC	CCTGTCCCAT	TGTGCTCCCT	CACATCTTCC	2666
273	ATTTCCCTCT	TTCTCCCTTA	GCCTCTTCTT	CCTCTTCTCT	TGTATCTCCC	2716
274	TTCCCTTTGC	TTCTCCCTCC	TCCTTTCCCC	TTCCCTATG	CCCTCTACTC	2766
275	TACTTGATCT	TCTCTCCTCT	CCACATACCC	TTTTTCCTTT	CCACCCTGCC	2816
276	CTTTGTCCCC	AGACCCTACA	GTATCCTGTG	CACAGGAAGT	GGGAGGTGCC	2866
277	ATCAACAACA	AGGAGGCAAG	AAACAGAGCA	AAATCCCAAA	ATCAGCAGGA	2916
278	AAGGCTGGAT	GAAAATAAGG	CCAGGTTCTG	AGGACAGCTG	GAATCTAGCC	2966
279	AAGTGGCTCC	TATAACCCTA	AGTACCAAGG	GAGAAAGTGA	TGGTGAAGTT	3016
280	CTTGATCCTT	GCTGCTTCTT	TTACATATGT	TGGCACATCT	TTCTCAAATG	3066
281	CAGGCCATGC	TCCATGCTTG	GCGCTTGCTC	AGCGTGGTTA	AGTAATGGGA	3116
282	GAATCTGAAA	ACTAGGGGCC	AGTGGTTTGT	TTTGGGGACA	AATTAGCAGC	3166
283	TAGTGATATT	TCCCCGTAAA	AATTATAACA	AACAGATTCA	TGATTTGAGA	3216
284	TCCTTCTACA	GGTGAGAAGT	GGAAAAATTG	TCACTATGAA	GTTCTTTTTA	3266
285	GGCTAAAGAT	ACTTGAACCC	ATAGAAGCGT	TGTTAAAATA	CTGCTTTCTT	3316
286	TTGCTAAAT	ATTCTTTCTC	ACATATTCAT	ATTCTCCAG		3355
287	GT GTT CCT	GGC CAT CAT	TTA AGG AAG	AAT GAA GTG	AAG TGT	3396
288	AGG ATG ATT	TAT TTC TTC	CAC GAC CCT	AAT TTC CTG	GTG TCT	3438
289	ATA CCA GTG	AAC CCT AAG	GAA CAA ATG	GAG TGT AGG	TGT GAA	3480
290	AAT GCT GAT	GAA GAG GTT	GCA ATG GAA	GAG GAA GAA	GAA GAA GAA	3522
291	GAG GAG GAG	GAG GAG GAA	GAG GAA ATG	GGA AAC CCG	GAT GGC	3564
292	TTC TCA CCT	TAG				3576
293	GCATGCAGGT	ACTGGCTTCA	CTAACCAACC	ATTCTTAACA	TATGCCTGTA	3626
294	GCTAAGAGCA	TCTTTTTTAA	AAATATTATT	GGTAAACTAA	ACAATTGTTA	3676
295	TCTTTTTTACA	TTAATAAGTA	TTAAATTAAT	CCAGTATACA	GTTTTAAGAA	3726
296	CCCTAAGTTA	AACAGAAGTC	AATGATGTCT	AGATGCCTGT	TCTTTAGATT	3776
297	GTAGTGAGAC	TACTTACTAC	AGATGAGAAG	TTGTTAGACT	CGGGAGTAGA	3826
298	GACCAGTAAA	AGATCATGCA	GTGAAATGTG	GCCATGGAAA	TCGCATATTG	3876
299	TTCTTATAGT	ACCTTTGAGA	CAGCTGATAA	CAGCTGACAA	AAATAAGTGT	3926
300	TTCAAGAAAG	ATCACACGCC	ATGGTTTACA	TGCAAAATTAT	TATTTTGTCTG	3976
301	TTCTGATTTT	TTTCATTTCT	AGACCTGTGG	TTTTAAAGAG	ATGAAAATCT	4026
302	CTTAAATTTT	CCTTCATCTT	TAATTTTCCT	TAACTTTAGT	TTTTTTCACT	4076
303	TAGAATTCAA	TTCAAATTCT	TAATTCAATC	TTAATTTTTA	GATTTCTTAA	4126
304	AATGTTTTTT	AAAAAAAATG	CAAATCTCAT	TTTAAAGAGA	TGAAAGCAGA	4176
305	GTAAGTGGGG	GGCTTAGGGA	ATCTGTAGGG	TTGCGGTATA	GCAATAGGGA	4226
306	GTTCTGGTCT	CTGAGAAGCA	GTCAGAGAGA	ATGGAAAACC	AGGCCCTTGC	4276
307	CAGTAGGTTA	GTGAGGTTGA	TATGATCAGA	TTATGGACAC	TCTCCAAATC	4326
308	ATAAATACTC	TAACAGCTAA	GGATCTCTGA	GGGAAACACA	ACAGGGAAAT	4376
309	ATTTTAGTTT	CTCCTTGAGA	AACAATGACA	AGACATAAAA	TTGGCAAGAA	4426
310	AGTCAGGAGT	GTATTCTAAT	AAGTGTGCT	TATCTCTTAT	TTTCTTCTAC	4476
311	AGTTGCAAAG	CCCAGAAGAA	AGAAATGGAC	AGCGGAAGAA	GTGGTTGTTT	4526
312	TTTTTTCCCC	TTCTTAATT	TTCTAGTTTT	TAGTAATCCA	GAAAATTGTA	4576
313	TTTTGTTCTA	AAGTTCAATTA	TGCAAAGATG	TCACCAACAG	ACTTCTGACT	4626
314	GCATGGTGAA	CTTTCATATG	ATACATAGGA	TTACACTTGT	ACCTGTTAAA	4676
315	AATAAAAGTT	TGACTTGCAT	AC			4698

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318 (2) INFORMATION FOR SEQUENCE ID NO: 6:

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319 (i) SEQUENCE CHARACTERISTICS:
320 (A) LENGTH: 7 amino acids
321 (B) TYPE: amino acid
322 (C) STRANDEDNESS: singular
323 (D) TOPOLOGY: linear
324 (ii) MOLECULE TYPE: protein
325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
326
327
328
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330 Leu Pro Tyr Leu Gly Trp Leu
331 5
332
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339 (2) INFORMATION FOR SEQUENCE ID NO: 7:
340 (i) SEQUENCE CHARACTERISTICS:
341 (A) LENGTH: 2419 base pairs
342 (B) TYPE: nucleic acid
343 (C) STRANDEDNESS: singular
344 (D) TOPOLOGY: linear
345 (ii) MOLECULE TYPE: genomic DNA
346 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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351	GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG	50
352	GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC	100
353	TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG	150
354	GGCCCGTGGA TTCCTCTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT	200
355	TGGTCTGAGA CAGTATCCTC AGGTACAGA GCAGAGGATG CACAGGGTGT	250
356	GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA	300
357	CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT	350
358	CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCCTGAGT ACCCTCTCAC	400
359	TTCCTCCTTC AGGTTTTTTCAG GGGACAGGCC AACCAGAGG ACAGGATTCC	450
360	CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTTG	500
361	TTAGAGTCTC CAAGGTTTCAG TTCTCAGCTG AGGCCTCTCA CACACTCCCT	550
362	CTCTCCCCAG GCCTGTGGGT CTTATTGCC CAGCTCCTGC CCACACTCCT	600
363	GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC	650
364	ACTGCAAGCC TGAGGAAGCC CTTGAGGCCC AACAAGAGGC CCTGGGCCTG	700
365	GTGTGTGTGC AGGCTGCCAC CTCCTCCTCC TCTCCTCTGG TCCTGGGCAC	750
366	CCTGGAGGAG GTGCCCCATG CTGGGTCAAC AGATCCTCCC CAGAGTCTC	800
367	AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA	850
368	CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG	900
369	TATCCTGGAG TCCTTGTTCC GAGCAGTAAT CACTAAGAAG GTGGCTGATT	950
370	TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG	1000
371	GCAGAAATGC TGGAGAGTGT CATCAAAAAT TACAAGCACT GTTTTCCTGA	1050

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372 GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG 1100
373 TGAAGGAAGC AGACCCACCC GGCCACTCCT ATGTCCTTGT CACCTGCCTA 1150
374 GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC 1200
375 AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GCGGGCCATG 1250
376 CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT 1300
377 GGGAGGGAGC ACAGTGCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA 1350
378 TTTGGTGCAG GAAAAGTACC TGGAGTACGG CAGGTGCCGG ACAGTGATCC 1400
379 CGCACGCTAT GAGTTCCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAGCT 1450
380 ATGTGAAAGT CCTTGAGTAT GTGATCAAGG TCAGTGCAAG AGTTCGCTTT 1500
381 TTCTTCCCAT CCCTGCGTGA AGCAGCTTTG AGAGAGGAGG AAGAGGGAGT 1550
382 CTGAGCATGA GTTGCAGCCA AGGCCAGTGG GAGGGGGACT GGGCCAGTGC 1600
383 ACCTTCCAGG GCCGCGTCCA GCAGCTTCCC CTGCCTCGTG TGACATGAGG 1650
384 CCCATTCTTC ACTCTGAAGA GAGCGGTGAG TGTTCTCAGT AGTAGGTTTC 1700
385 TGTTCTATTG GGTGACTTGG AGATTTATCT TTGTTCTCTT TTGGAATTGT 1750
386 TCAAATGTTT TTTTAAAGG GATGGTTGAA TGAAGTTCAG CATCCAAGTT 1800
387 TATGAATGAC AGCAGTCACA CAGTTCCTGT TATATAGTTT AAGGGTAAGA 1850
388 GTCTTGTGTT TTATTCAGAT TGGGAATAGC ATTCTATTTT GTGAATTGGG 1900
389 ATAATAACAG CAGTGGGAATA AGTAACTAGA AATGTGAAAA ATGAGCAGTA 1950
390 AAATAGATGA GATAAAGAAC TAAAGAAATT AAGAGATAGT CAATTCTTGC 2000
391 CTTATACCTC AGTCTATTCT GTAAAATTTT TAAAGATATA TGCATACCTG 2050
392 GATTTCTTGG GCTTCTTTGA GAATGTAAGA GAAATTAAAT CTGAATAAAG 2100
393 AATTCTTCCT GTTCACTGGC TCTTTTCTTC TCCATGCACT GAGCATCTGC 2150
394 TTTTGGGAAG GCCCTGGGTT AGTAGTGGAG ATGCTAAGGT AAGCCAGACT 2200
395 CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG 2250
396 AGGTGGCAAG ATGTCCTCTA AAGATGTAGG GAAAAGTGAG AGAGGGGTGA 2300
397 GGGTGTGGGG CTCCGGGTGA GAGTGGTGGA GTGTCAATGC CCTGAGCTGG 2350
398 GGCATTTTGG GCTTTGGGAA ACTGCAGTTC CTTCTGGGGG AGCTGATTGT 2400
399 AATGATCTTG GGTGGATCC 2419
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400
401 (2) INFORMATION FOR SEQUENCE ID NO: 8:
402 (i) SEQUENCE CHARACTERISTICS:
403 (A) LENGTH: 5674 base pairs
404 (B) TYPE: nucleic acid
405 (C) STRANDEDNESS: singular
406 (D) TOPOLOGY: linear
407 (ii) MOLECULE TYPE: genomic DNA
408 (ix) FEATURE:
409 (A) NAME/KEY: MAGE-1 gene
410 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
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412
413
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414 CCCGGGGCAC CACTGGCATC CCTCCCCCTA CCACCCCAAA TCCCTCCCTT 50
415 TACGCCACCC ATCCAAACAT CTTACGCTC ACCCCAGCC CAAGCCAGGC 100
416 AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGCCC AGGTGCCCAG 150
417 ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTTT 200
418 CGGTCTGAGG GCGGCTTGA GATCGGTGGA GGAAGCGGG CCCAGCTCTG 250
419 TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACC CACTTACCCC 300
420 AGATAGAGGA CCCCATAATA TCCCTTCATG CCAGTCCTGG ACCATCTGGT 350
421 GGTGGACTTC TCAGGCTGGG CCACCCCAAG CCCCTTGCT GCTTAAACCA 400
422 CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGAAGG GCTGCTTAGG 450
423 AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG 500
424 AGGGCTGAGG GTCCCTAAGA CCCCCTCCC GTGACCCAAC CCCCCTCCA 550
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425	ATGCTCACTC	CCGTGACCCA	ACCCCCTCTT	CATTGTCATT	CCAACCCCCA	600
426	CCCCACATCC	CCCACCCCAT	CCCTCAACCC	TGATGCCCAT	CCGCCCAGCC	650
427	ATTCCACCCT	CACCCCCACC	CCCACCCCCA	CGCCCACTCC	CACCCCCACC	700
428	CAGGCAGGAT	CCGGTTCCCG	CCAGGAAACA	TCCGGGTGCC	CGGATGTGAC	750
429	GCCACTGACT	TGCGCATTGT	GGGGCAGAGA	GAAGCGAGGT	TTCCATTCTG	800
430	AGGGACGGCG	TAGAGTTCCG	CCGAAGGAAC	CTGACCCAGG	CTCTGTGAGG	850
431	AGGCAAGGTG	AGAGGCTGAG	GGAGGACTGA	GGACCCCGCC	ACTCCAAATA	900
432	GAGAGCCCCA	AATATTCCAG	CCCCGCCCTT	GCTGCCAGCC	CTGGCCCACC	950
433	CGCGGGAAGA	CGTCTCAGCC	TGGGCTGCCC	CCAGACCCCT	GCTCCAAAAG	1000
434	CCTTGAGAGA	CACCAGGTTT	TTCTCCCCAA	GCTCTGGAAT	CAGAGGTTGC	1050
435	TGTGACCAGG	GCAGGACTGG	TTAGGAGAGG	GCAGGGCACA	GGCTCTGCCA	1100
436	GGCATCAAGA	TCAGCACCCA	AGAGGGAGGG	CTGTGGGCCC	CCAAGACTGC	1150
437	ACTCCAATCC	CCACTCCCAC	CCCATTGCGA	TTCCCATTC	CCACCCAACC	1200
438	CCCATCTCCT	CAGCTACACC	TCCACCCCCA	TCCCTACTCC	TACTCCGTCA	1250
439	CCTGACCACC	ACCCTCCAGC	CCCAGCACCA	GCCCCAACCC	TTCTGCCACC	1300
440	TCACCCCTAC	TGCCCCCAAC	CCCACCCTCA	TCTCTCTCAT	GTGCCCCACT	1350
441	CCCATCGCCT	CCCCATTCT	GGCAGAATCC	GGTTTGCCCC	TGCTCTCAAC	1400
442	CCAGGGAAGC	CCTGGTAGGC	CCGATGTGAA	ACCATGACT	TGAACCTCAC	1450
443	AGATCTGAGA	GAAGCCAGGT	TCATTTAATG	GTTCTGAGGG	GCGGCTTGAG	1500
444	ATCCACTGAG	GGGAGTGGTT	TTAGGCTCTG	TGAGGAGGCA	AGGTGAGATG	1550
445	CTGAGGGAGG	ACTGAGGAGG	CACACACCCC	AGGTAGATGG	CCCCAAAATG	1600
446	ATCCAGTACC	ACCCTTGCTG	CCAGCCCTGG	ACCACCCGGC	CAGGACAGAT	1650
447	GTCTCAGCTG	GACCACCCCC	CGTCCCGTCC	CACTGCCACT	TAACCCACAG	1700
448	GGCAATCTGT	AGTCATAGCT	TATGTGACCG	GGGCAGGGTT	GGTCAGGAGA	1750
449	GGCAGGGCCC	AGGCATCAAG	GTCCAGCATC	CGCCCGGCAT	TAGGGTCAGG	1800
450	ACCCTGGGAG	GGAACTGAGG	GTTCCCCACC	CACACCTGTC	TCCTCATCTC	1850
451	CACCGCCACC	CCACTCACAT	TCCCATACTT	ACCCCCTACC	CCCAACCTCA	1900
452	TCTTGTCAGA	ATCCCTGCTG	TCAACCCACG	GAAGCCACGG	GAATGGCGGC	1950
453	CAGGCACTCG	GATCTTGACG	TCCCCATCCA	GGGTCTGATG	GAGGGAAGGG	2000
454	GCTTGAACAG	GGCCTCAGGG	GAGCAGAGGG	AGGGCCCTAC	TGCGAGATGA	2050
455	GGGAGGCCTC	AGAGGACCCA	GCACCCTAGG	ACACCGCACC	CCTGTCTGAG	2100
456	ACTGAGGCTG	CCACTTCTGG	CCTCAAGAAT	CAGAACGATG	GGGACTCAGA	2150
457	TTGCATGGGG	GTGGGACCCA	GGCCTGCAAG	GCTTACGCGG	AGGAAGAGGA	2200
458	GGGAGGACTC	AGGGGACCTT	GGAATCCAGA	TCAGTGTGGA	CCTCGGCCCT	2250
459	GAGAGGTCCA	GGGCACGGTG	GCCACATATG	GCCCATATTT	CCTGCATCTT	2300
460	TGAGGTGACA	GGACAGAGCT	GTGGTCTGAG	AAGTGGGGCC	TCAGGTCAAC	2350
461	AGAGGGAGGA	GTTCCAGGAT	CCATATGGCC	CAAGATGTGC	CCCCTTCATG	2400
462	AGGACTGGGG	ATATCCCCGG	CTCAGAAAGA	AGGGACTCCA	CACAGTCTGG	2450
463	CTGTCCCCTT	TTAGTAGCTC	TAGGGGGACC	AGATCAGGGA	TGGCGGTATG	2500
464	TTCCATTCTC	ACTTGTACCA	CAGGCAGGAA	GTTGGGGGGC	CCTCAGGGAG	2550
465	ATGGGGTCTT	GGGGTAAAGG	GGGGATGTCT	ACTCATGTCA	GGGAATTGGG	2600
466	GGTTGAGGAA	GCACAGGCGC	TGGCAGGAAT	AAAGATGAGT	GAGACAGACA	2650
467	AGGCTATTGG	AATCCACACC	CCAGAACCAA	AGGGGTCAGC	CCTGGACACC	2700
468	TCACCCAGGA	TGTGGCTTCT	TTTTCACTCC	TGTTTCCAGA	TCTGGGGCAG	2750
469	GTGAGGACCT	CATTCTCAGA	GGGTGACTCA	GGTCAACGTA	GGGACCCCCA	2800
470	TCTGGTCTAA	AGACAGAGCG	GTCCCAGGAT	CTGCCATGCG	TTCGGGTGAG	2850
471	GAACATGAGG	GAGGACTGAG	GGTACCCAG	GACCAGAACA	CTGAGGGAGA	2900
472	CTGCACAGAA	ATCAGCCCTG	CCCCTGCTGT	CACCCAGAG	AGCATGGGCT	2950
473	GGGCCGTCTG	CCGAGGTCCT	TCCGTTATCC	TGGGATCATT	GATGTCAGGG	3000
474	ACGGGGAGGC	CTTGGTCTGA	GAAGGCTGCG	CTCAGGTCAG	TAGAGGGAGC	3050
475	GTCCCAGGCC	CTGCCAGGAG	TCAAGGTGAG	GACCAAGCGG	GCACCTCACC	3100
476	CAGGACACAT	TAATTCCAAT	GAATTTTGAT	ATCTCTTGCT	GCCCTTCCCC	3150
477	AAGGACCTAG	GCACGTGTGG	CCAGATGTTT	GTCCCTCCT	GTCCTTCCAT	3200

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478	TCCTTATCAT	GGATGTGAAC	TCTTGATTG	GATTTCTCAG	ACCAGCAAAA	3250
479	GGGCAGGATC	CAGGCCCTGC	CAGGAAAAAT	ATAAGGGCCC	TGCGTGAGAA	3300
480	CAGAGGGGGT	CATCCACTGC	ATGAGAGTGG	GGATGTCACA	GAGTCCAGCC	3350
481	CACCCCTCCTG	GTAGCACTGA	GAAGCCAGGG	CTGTGCTTGC	GGTCTGCACC	3400
482	CTGAGGGCCC	GTGGATTCCCT	CTTCCTGGAG	CTCCAGGAAC	CAGGCAGTGA	3450
483	GGCCTTGGTC	TGAGACAGTA	TCCTCAGGTC	ACAGAGCAGA	GGATGCACAG	3500
484	GGTGTGCCAG	CAGTGAATGT	TTGCCCTGAA	TGCACACCAA	GGGCCCCACC	3550
485	TGCCACAGGA	CACATAGGAC	TCCACAGAGT	CTGGCCTCAC	CTCCCTACTG	3600
486	TCAGTCCTGT	AGAATCGACC	TCTGCTGGCC	GGCTGTACCC	TGAGTACCCT	3650
487	CTCACTTCCT	CCTTCAGGTT	TTCAGGGGAC	AGGCCAACCC	AGAGGACAGG	3700
488	ATTCCCTGGA	GGCCACAGAG	GAGCACCAAG	GAGAAGATCT	GTAAGTAGGC	3750
489	CTTTGTTAGA	GTCTCCAAGG	TTCACTTCTC	AGCTGAGGCC	TCTCACACAC	3800
490	TCCCTCTCTC	CCCAGGCCTG	TGGGTCTTCA	TTGCCCAGCT	CCTGCCCACA	3850
491	CTCCTGCCTG	CTGCCCTGAC	GAGAGTCATC			3880
492	ATG TCT CTT	GAG CAG AGG	AGT CTG CAC	TGC AAG CCT	GAG GAA	3922
493	GCC CTT GAG	GCC CAA CAA	GAG GCC CTG	GGC CTG GTG	TGT GTG	3964
494	CAG GCT GCC	ACC TCC TCC	TCT CCT CTG	GTC CTG GGC	ACC	4006
495	CTG GAG GAG	GTG CCC ACT	GCT GGG TCA	ACA GAT CCT	CCC CAG	4048
496	AGT CCT CAG	GGA GCC TCC	GCC TTT CCC	ACT ACC ATC	AAC TTC	4090
497	ACT CGA CAG	AGG CAA CCC	AGT GAG GGT	TCC AGC AGC	CGT GAA	4132
498	GAG GAG GGG	CCA AGC ACC	TCT TGT ATC	CTG GAG TCC	TTG TTC	4174
499	CGA GCA GTA	ATC ACT AAG	AAG GTG GCT	GAT TTG GTT	GGT TTT	4216
500	CTG CTC CTC	AAA TAT CGA	GCC AGG GAG	CCA GTC ACA	AAG GCA	4258
501	GAA ATG CTG	GAG AGT GTC	ATC AAA AAT	TAC AAG CAC	TGT TTT	4300
502	CCT GAG ATC	TTC GGC AAA	GCC TCT GAG	TCC TTG CAG	CTG GTC	4342
503	TTT GGC ATT	GAC GTG AAG	GAA GCA GAC	CCC ACC GGC	CAC TCC	4384
504	TAT GTC CTT	GTC ACC TGC	CTA GGT CTC	TCC TAT GAT	GGC CTG	4426
505	CTG GGT GAT	AAT CAG ATC	ATG CCC AAG	ACA GGC TTC	CTG ATA	4468
506	ATT GTC CTG	GTC ATG ATT	GCA ATG GAG	GGC GGC CAT	GCT CCT	4510
507	GAG GAG GAA	ATC TGG GAG	GAG CTG AGT	GTG ATG GAG	GTG TAT	4552
508	GAT GGG AGG	GAG CAC AGT	GCC TAT GGG	GAG CCC AGG	AAG CTG	4594
509	CTC ACC CAA	GAT TTG GTG	CAG GAA AAG	TAC CTG GAG	TAC GGC	4636
510	AGG TGC CGG	ACA GTG ATC	CCG CAC GCT	ATG AGT TCC	TGT GGG	4678
511	GTC CAA GGG	CCC TCG CTG	AAA CCA GCT	ATG TGA		4711
512	AAGTCCTTGA	GTATGTGATC	AAGGTCAGTG	CAAGAGTTC		4750
513	GCTTTTTCTT	CCCATCCCTG	CGTGAAGCAG	CTTTGAGAGA	GGAGGAAGAG	4800
514	GGAGTCTGAG	CATGAGTTGC	AGCCAAGGCC	AGTGGGAGGG	GGACTGGGCC	4850
515	AGTGCACCTT	CCAGGGCCGC	GTCCAGCAGC	TTCCCTGCC	TCGTGTGACA	4900
516	TGAGGCCCAT	TCTTCACTCT	GAAGAGAGCG	GTCAGTGTTT	TCAGTAGTAG	4950
517	GTTTCTGTTC	TATTGGGTGA	CTTGGAGATT	TATCTTTGTT	CTCTTTTGGA	5000
518	ATTGTTCAAA	TGTTTTTTTT	TAAGGGATGG	TTGAATGAAC	TTCAGCATCC	5050
519	AAGTTTATGA	ATGACAGCAG	TCACACAGTT	CTGTGTATAT	AGTTTAAGGG	5100
520	TAAGAGTCTT	GTGTTTTATT	CAGATTGGGA	AATCCATTCT	ATTTTGTGAA	5150
521	TTGGGATAAT	AACAGCAGTG	GAATAAGTAC	TTAGAAATGT	GAAAAATGAG	5200
522	CAGTAAAATA	GATGAGATAA	AGAACTAAAG	AAATTAAGAG	ATAGTCAATT	5250
523	CTTGCCTTAT	ACCTCAGTCT	ATTCTGTAAA	ATTTTAAAG	ATATATGCAT	5300
524	ACCTGGATTT	CCTTGGCTTC	TTTGAGAATG	TAAGAGAAAT	TAAATCTGAA	5350
525	TAAAGAATTC	TTCTGTGTTA	CTGGCTCTTT	TCTTCTCCAT	GCACTGAGCA	5400
526	TCTGCTTTTT	GGAGGGCCCT	GGGTTAGTAG	TGGAGATGCT	AAGGTAAGCC	5450
527	AGACTCATAC	CCACCCATAG	GGTCGTAGAG	TCTAGGAGCT	GCAGTCACGT	5500
528	AATCGAGGTG	GCAAGATGTC	CTCTAAAGAT	GTAGGGAAAA	GTGAGAGAGG	5550
529	GGTGAGGGTG	TGGGGCTCCG	GGTGAGAGTG	GTGGAGTGTC	AATGCCCTGA	5600
530	GCTGGGGCAT	TTTGGGCTTT	GGGAACTGC	AGTTCCTTCT	GGGGGAGCTG	5650

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531 ATTGTAATGA TCTTGGGTGG ATCC

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536 (2) INFORMATION FOR SEQUENCE ID NO: 9:

537 (i) SEQUENCE CHARACTERISTICS:

538 (A) LENGTH: 4157 base pairs

539 (B) TYPE: nucleic acid

540 (C) STRANDEDNESS: singular

541 (D) TOPOLOGY: linear

542 (ii) MOLECULE TYPE: genomic DNA

543 (ix) FEATURE:

544 (A) NAME/KEY: MAGE-2 gene

545 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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549 CCCATCCAGA TCCCCATCCG GGCAGAATCC GGTTCACCCC TTGCCGTGAA 50

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551 GGTTCAGAGGA CAGCGAGATT CTCGCCCTGA GCAACGGCCT GACGTCGGCG 150

552 GAGGGAAGCA GCGCGAGGCT CCGTGAGGAG GCAAGGTAAG ACGCCGAGGG 200

553 AGGACTGAGG CGGGCCTCAC CCCAGACAGA GGGCCCCCAA TTAATCCAGC 250

554 GCTGCCTCTG CTGCCGGGCC TGGACCACCC TGCAGGGGAA GACTTCTCAG 300

555 GCTCAGTCGC CACCACCTCA CCCC GCCACC CCCC GCCGCT TTAACCGCAG 350

556 GGAACCTCTG CGTAAGAGCT TTGTGTGACC AGGGCAGGGC TGGTTAGAAG 400

557 TGCTCAGGGC CCAGACTCAG CCAGGAATCA AGGTCAGGAC CCCAAGAGGG 450

558 GACTGAGGGC AACCCACCCC CTACCCTCAC TACCAATCCC ATCCCCAAC 500

559 ACCAACCCCA CCCCCATCCC TCAAACACCA ACCCCACCCC CAAACCCCAT 550

560 TCCCATCTCC TCCCCACCA CCATCCTGGC AGAATCCGGC TTTGCCCTG 600

561 CAATCAACCC ACGGAAGCTC CGGGAATGGC GGCCAAGCAC GCGGATCCTG 650

562 ACGTTACAT GTACGGCTAA GGGAGGGAAG GGGTTGGGTC TCGTGAGTAT 700

563 GGCCTTTGGG ATGCAGAGGA AGGGCCAGG CCTCTGGAA GACAGTGGAG 750

564 TCCTTAGGGG ACCCAGCATG CCAGGACAGG GGGCCCACTG TACCCCTGTC 800

565 TCAAAGTGAG CCACCTTTTC ATTCAGCCGA GGGAAATCCTA GGGATGCAGA 850

566 CCCACTTCAG GGGGTTGGGG CCCAGCCTGC GAGGAGTCAA GGGGAGGAAG 900

567 AAGAGGGAGG ACTGAGGGGA CCTTGGAGTC CAGATCAGTG GCAACCTTGG 950

568 GCTGGGGGAT CCTGGGCACA GTGGCCGAAT GTGCCCCGTG CTCATTGCAC 1000

569 CTTCAGGGTG ACAGAGAGTT GAGGGCTGTG GTCTGAGGGC TGGGACTTCA 1050

570 GGTCAGCAGA GGGAGGAATC CCAGGATCTG CCGGACCCAA GGTGTGCCCC 1100

571 CTTTCATGAGG ACTCCCCATA CCCCCGGCCC AGAAAGAAGG GATGCCACAG 1150

572 AGTCTGGAAG TAAATTGTTC TTAGCTCTGG GGGAACTGA TCAGGGATGG 1200

573 CCCTAAGTGA CAATCTCATT TGTACCACAG GCAGGAGGTT GGGGAACCCT 1250

574 CAGGGAGATA AGGTGTTGGT GTAAAGAGGA GCTGTCTGCT CATTTAGGG 1300

575 GGTTCCCCTT TGAGAAAGGG CAGTCCCTGG CAGGAGTAAA GATGAGTAAC 1350

576 CCACAGGAGG CCATCATAAC GTTCACCCTA GAACCAAAGG GGTCAGCCCT 1400

577 GGACAACGCA CGTGGGGTAA CAGGATGTGG CCCCTCCTCA CTTGTCTTTC 1450

578 CAGATCTCAG GGAGTTGATG ACCTTGTTT CAGAAGGTGA CTCAGTCAAC 1500

579 ACAGGGGCCC CTCTGGTCGA CAGATGCAGT GGTTCTAGGA TCTGCCAAGC 1550

580 ATCCAGGTGG AGAGCCTGAG GTAGGATTGA GGGTACCCCT GGGCCAGAAT 1600

581 GCAGCAAGGG GGCCCCATAG AAATCTGCCC TGCCCCCTGC GTTACTTCAG 1650

582 AGACCCTGGG CAGGGCTGTC AGCTGAAGTC CCTCCATTAT CTGGGATCTT 1700

583 TGATGTCAGG GAAGGGGAGG CCTTGGTCTG AAGGGGCTGG AGTCAGGTCA 1750

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584	GTAGAGGGAG	GGTCTCAGGC	CCTGCCAGGA	GTGGACGTGA	GGACCAAGCG	1800
585	GACTCGTCAC	CCAGGACACC	TGGACTCCAA	TGAATTTGAC	ATCTCTCGTT	1850
586	GTCCTTCGCG	GAGGACCTGG	TCACGTATGG	CCAGATGTGG	GTCCCCCTCTA	1900
587	TCTCCTTCTG	TACCATATCA	GGGATGTGAG	TTCTTGACAT	GAGAGATTCT	1950
588	CAAGCCAGCA	AAAGGGTGGG	ATTAGGCCCT	ACAAGGAGAA	AGGTGAGGGC	2000
589	CCTGAGTGAG	CACAGAGGGG	ACCCTCCACC	CAAGTAGAGT	GGGGACCTCA	2050
590	CGGAGTCTGG	CCAACCCTGC	TGAGACTTCT	GGGAATCCGT	GGCTGTGCTT	2100
591	GCAGTCTGCA	CACTGAAGGC	CCGTGCATTC	CTCTCCCAGG	AATCAGGAGC	2150
592	TCCAGGAACC	AGGCAGTGAG	GCCTTGGTCT	GAGTCAGTGC	CTCAGGTCAC	2200
593	AGAGCAGAGG	GGACGCAGAC	AGTGCCAACA	CTGAAGGTTT	GCCTGGAATG	2250
594	CACACCAAGG	GCCCCACCCG	CCCAGAACAA	ATGGGACTCC	AGAGGGCCTG	2300
595	GCCTCACCCCT	CCCTATTCTC	AGTCCTGCAG	CCTGAGCATG	TGCTGGCCGG	2350
596	CTGTACCCTG	AGGTGCCCTC	CCACTTCCTC	CTTCAGGTTC	TGAGGGGGAC	2400
597	AGGCTGACAA	GTAGGACCCG	AGGCACTGGA	GGAGCATTGA	AGGAGAAGAT	2450
598	CTGTAAGTAA	GCCTTTGTCA	GAGCCTCCAA	GGTTCAGTTC	AGTTCTCACC	2500
599	TAAGGCCTCA	CACACGCTCC	TTCTCTCCCC	AGGCCTGTGG	GTCTTCATTG	2550
600	CCCAGCTCCT	GCCCCGACTC	CTGCCCTGCTG	CCCTGACCAG	AGTCATC	2597
601	ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	2639
602	GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG GTG	GGT GCG	2681
603	CAG GCT CCT	GCT ACT GAG	GAG CAG CAG	ACC GCT TCT	TCC TCT	2723
604	TCT ACT CTA	GTG GAA GTT	ACC CTG GGG	GAG GTG CCT	GCT GCC	2765
605	GAC TCA CCG	AGT CCT CCC	CAC AGT CCT	CAG GGA GCC	TCC AGC	2807
606	TTC TCG ACT	ACC ATC AAC	TAC ACT CTT	TGG AGA CAA	TCC GAT	2849
607	GAG GGC TCC	AGC AAC CAA	GAA GAG GAG	GGG CCA AGA	ATG TTT	2891
608	CCC GAC CTG	GAG TCC GAG	TTC CAA GCA	GCA ATC AGT	AGG AAG	2933
609	ATG GTT GAG	TTG GTT CAT	TTT CTG CTC	CTC AAG TAT	CGA GCC	2975
610	AGG GAG CCG	GTC ACA AAG	GCA GAA ATG	CTG GAG AGT	GTC CTC	3017
611	AGA AAT TGC	CAG GAC TTC	TTT CCC GTG	ATC TTC AGC	AAA GCC	3059
612	TCC GAG TAC	TTG CAG CTG	GTC TTT GGC	ATC GAG GTG	GTG GAA	3101
613	GTG GTC CCC	ATC AGC CAC	TTG TAC ATC	CTT GTC ACC	TGC CTG	3143
614	GGC CTC TCC	TAC GAT GGC	CTG CTG GGC	GAC AAT CAG	GTC ATG	3185
615	CCC AAG ACA	GGC CTC CTG	ATA ATC GTC	CTG GCC ATA	ATC GCA	3227
616	ATA GAG GGC	GAC TGT GCC	CCT GAG GAG	AAA ATC TGG	GAG GAG	3269
617	CTG AGT ATG	TTG GAG GTG	TTT GAG GGG	AGG GAG GAC	AGT GTC	3311
618	TTC GCA CAT	CCC AGG AAG	CTG CTC ATG	CAA GAT CTG	GTG CAG	3353
619	GAA AAC TAC	CTG GAG TAC	CGG CAG GTG	CCC GGC AGT	GAT CCT	3395
620	GCA TGC TAC	GAG TTC CTG	TGG GGT CCA	AGG GCC CTC	ATT GAA	3437
621	ACC AGC TAT	GTG AAA GTC	CTG CAC CAT	ACA CTA AAG	ATC GGT	3479
622	GGA GAA CCT	CAC ATT TCC	TAC CCA CCC	CTG CAT GAA	CGG GCT	3521
623	TTG AGA GAG	GGA GAA GAG	TGA			3542
624	GTCTCAGCAC	ATGTTGCAGC	CAGGGCCAGT	GGGAGGGGGT	CTGGGCCAGT	3592
625	GCACCTTCCA	GGGCCCCATC	CATTAGCTTC	CACTGCCTCG	TGTGATATGA	3642
626	GGCCCATTC	TGCCCTTTG	AAGAGAGCAG	TCAGCATTCT	TAGCAGTGAG	3692
627	TTTCTGTTCT	GTTGGATGAC	TTTGAGATTT	ATCTTTCTTT	CCTGTTGGAA	3742
628	TTGTTCAAAT	GTTCCTTTTA	ACAAATGGTT	GGATGAACTT	CAGCATCCAA	3792
629	GTTTATGAAT	GACAGTAGTC	ACACATAGTG	CTGTTTATAT	AGTTTAGGGG	3842
630	TAAGAGTCTT	GTTTTTTATT	CAGATTGGGA	AATCCATTCC	ATTTTGTGAG	3892
631	TTGTCACATA	ATAACAGCAG	TGGAATATGT	ATTTGCCCTAT	ATTGTGAACG	3942
632	AATTAGCAGT	AAAATACATG	ATACAAGGAA	CTCAAAAGAT	AGTTAATTCT	3992
633	TGCCTTATAC	CTCAGTCTAT	TATGTAAAAT	TAAAAATATG	TGTATGTTTT	4042
634	TGCTTCTTTG	AGAATGCAAA	AGAAATTAAA	TCTGAATAAA	TTCTTCCTGT	4092
635	TCACTGGCTC	ATTTCTTTAC	CATTCACCTCA	GCATCTGCTC	TGTGGAAGGC	4142
636	CCTGGTAGTA	GTGGG				4157

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(2) INFORMATION FOR SEQUENCE ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-21 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGATCCCCAT	GGATCCAGGA	AGAATCCAGT	TCCACCCCTG	CTGTGAACCC	50
AGGGAAGTCA	CGGGGCCGGA	TGTGACGCCA	CTGACTTGCG	CGTTGGAGGT	100
CAGAGAACAG	CGAGATTCTC	GCCCTGAGCA	ACGGCCTGAC	GTCGGCGGAG	150
GGAAGCAGGC	GCAGGCTCCG	TGAGGAGGCA	AGGTAAGATG	CCGAGGGAGG	200
ACTGAGGCGG	GCCTCACCCC	AGACAGAGGG	CCCCCAATAA	TCCAGCGCTG	250
CCTCTGCTGC	CAGGCCTGGA	CCACCCTGCA	GGGGAAGACT	TCTCAGGCTC	300
AGTCGCCACC	ACCTCACCCC	GCCACCCCCC	GCCGCTTTAA	CCGCAGGGAA	350
CTCTGGTGTA	AGAGCTTTGT	GTGACCAGGG	CAGGGCTGGT	TAGAAGTGCT	400
CAGGGCCAG	ACTCAGCCAG	GAATCAAGGT	CAGGACCCCA	AGAGGGGACT	450
GAGGGTAACC	CCCCCGCACC	CCCACCACCA	TTCCCATCCC	CCAACACCAA	500
CCCCACCCCC	ATCCCCCAAC	ACCAAACCCA	CCACCATCGC	TCAAACATCA	550
ACGGCACCCC	CAAACCCCGA	TTCCCATCCC	CACCCATCCT	GGCAGAATCG	600
GAGCTTTGCC	CCTGCAATCA	ACCCACGGAA	GCTCCGGGAA	TGGCGGCCAA	650
GCACGCGGAT	CC				662

(2) INFORMATION FOR SEQUENCE ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: cDNA MAGE-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

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690
691 GCCGCGAGGG AAGCCGGCCCC AGGCTCGGTG AGGAGGCAAG GTTCTGAGGG 50
692 GACAGGCTGA CCTGGAGGAC CAGAGGCCCC CGGAGGAGCA CTGAAGGAGA 100
693 AGATCTGCCA GTGGGTCTCC ATTGCCCAGC TCCTGCCCAC ACTCCCGCCT 150
694 GTTGCCCTGA CCAGAGTCAT C 171
695 ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA 213
696 GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG 255
697 CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT 297
698 TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC 339
699 GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC 381
700 CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT 423
701 GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC 465
702 CCT GAC CTG GAG TCC GAG TTC CAA GCA GCA CTC AGT AGG AAG 507
703 GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC 549
704 AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC 591
705 GGA AAT TGG CAG TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT 633
706 TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA 675
707 GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG 717
708 GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG 759
709 CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA 801
710 AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG 843
711 CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG 885
712 TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG 927
713 GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT 969
714 GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA 1011
715 ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT 1053
716 GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT 1095
717 TTG AGA GAG GGG GAA GAG TGA 1116
718 GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT 1166
719 GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCTCC TGTGACGTGA 1216
720 GGCCCATTTCT TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG 1266
721 TTTCTGTTCT GTTGGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG 1316
722 TTGTTCAAAT GTTCCTTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG 1366
723 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGAG 1416
724 TAAGAGTCTT GttTTTTACT CAAATTgGGA AATCCATTCC ATTTTGTGAA 1466
725 TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC 1516
726 GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG 1566
727 ATTCTTGCCT TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA 1616
728 ACCAGGATTT CCTTGACTTC TTG 1640

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733 (2) INFORMATION FOR SEQUENCE ID NO: 12:

734 (i) SEQUENCE CHARACTERISTICS:

735 (A) LENGTH: 943 base pairs

736 (B) TYPE: nucleic acid

737 (C) STRANDEDNESS: singular

738 (D) TOPOLOGY: linear

739 (ii) MOLECULE TYPE: genomic DNA

740 (ix) FEATURE:

741 (A) NAME/KEY: MAGE-31 gene

742 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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743
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746 GGATCCTCCA CCCAGTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT 50
747 CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG 100
748 GCCCGTGGAT TCCTCTCCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG 150
749 AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGgCTCA 200
750 GATAGTGCCA ACGGTGAAGG TTTGCCTTGG ATTCAAACCA AGGGCCCCAC 250
751 CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT 300
752 TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC 350
753 CTCTCACTTC CTCCTTCAGG TTCTGAGGGG ACAGGCTGAC CTGAGGACC 400
754 AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG 450
755 TTAGAGCCTC CAAGGTTCCA TTCAGTACTC AGCTGAGGTC TCTCACATGC 500
756 TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCAGCT CCTGCCCCACA 550
757 CTCCCGCCTG TTGCCCTGAC CAGAGTCATC 580
758 ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA 622
759 GGC CTT GAG GCC CGA GGA GAg GCC CTG GGC CTG GTG GGT GCG 664
760 CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT 706
761 TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC 748
762 GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC 790
763 CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT 832
764 GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC 874
765 CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG 916
766 GTG GCC AAG TTG GTT CAT TTT CTG CTC 943

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771 (2) INFORMATION FOR SEQUENCE ID NO: 13:

772 (i) SEQUENCE CHARACTERISTICS:

773 (A) LENGTH: 1067 base pairs

774 (B) TYPE: nucleic acid

775 (C) STRANDEDNESS: singular

776 (D) TOPOLOGY: linear

777 (ii) MOLECULE TYPE: cDNA to mRNA

778 (ix) FEATURE:

779 (A) NAME/KEY: cDNA MAGE-4

780 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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784 GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA 39
785 GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG 81
786 CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA 123
787 ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT 165
788 GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT 207
789 GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC 249
790 ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG 291
791 GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC 333
792 GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG 375
793 GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT 417
794 GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC 459
795 ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG 501

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796 GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT 543
797 CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG 585
798 CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA 627
799 TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC 669
800 TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG 719
801 TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG 769
802 GCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTT TTAGTAGTGG 819
803 GTTCTATTTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA 869
804 ATTGTTGAAA TGTTCTTTT AATGGATGGT TGAATTAAT TCAGCATCCA 919
805 AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTAATATA GTTTAGGAGT 969
806 AAGAGTCTTG TTTTATTC AGATTGGGAA ATCCGTCTA TTTGTGAAT 1019
807 TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC 1067
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810 (2) INFORMATION FOR SEQUENCE ID NO: 14:
811 (i) SEQUENCE CHARACTERISTICS:
812 (A) LENGTH: 226 base pairs
813 (B) TYPE: nucleic acid
814 (C) STRANDEDNESS: singular
815 (D) TOPOLOGY: linear
816 (ii) MOLECULE TYPE: genomic DNA
817 (ix) FEATURE:
818 (A) NAME/KEY: MAGE-5 gene
819 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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823 AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG ATCTGTAAGT 50
824 AAGCCTTTGT TAGAGCCTCC AAGGTTCAAGT TTTAGCTGA GGCTTCTCAC 100
825 ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC AGCTCCTGCC 150
826 CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC 184
827 ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 226
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829 (2) INFORMATION FOR SEQUENCE ID NO: 15:
830 (i) SEQUENCE CHARACTERISTICS:
831 (A) LENGTH: 225 base pairs
832 (B) TYPE: nucleic acid
833 (C) STRANDEDNESS: singular
834 (D) TOPOLOGY: linear
835 (ii) MOLECULE TYPE: cDNA
836 (ix) FEATURE:
837 (A) NAME/KEY: MAGE-6 gene
838 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
839
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842 TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG 42
843 CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC 84
844 GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC 126
845 GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC 168
846 TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC 210
847 TGT GCC CCT GAG GAG 225
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- (2) INFORMATION FOR SEQUENCE ID NO: 16:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (ix) FEATURE:
- (A) NAME/KEY: MAGE-7 gene
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ACA AGC ACT AGT TTC CTT GTG ATC TAT GGC AAA GCC TCA GAG	42
TGC ATG CAG GTG ATG TTT GGC ATT GAC ATG AAG GAA GTG GAC	84
CCC GCG GCC ACT CCT ACG TCT TGT ACC TGC TTG GGC CTC TCC	126
TAC AAT GGC CTG CTG GGT GAT GAT CAG AGC ATG CCC GAG A	166

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/807,043B

DATE: 11/06/92
TIME: 14:38:15

LINE ERROR

ORIGINAL TEXT

24 Wrong application Serial Number

(A) APPLICATION NUMBER: 07/807,043



PAGE:

1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/807,043B

DATE: 11/06/92
TIME: 14:38:15

MANDATORY IDENTIFIER THAT WAS NOT FOUND

COUNTRY

LINE ORIGINAL TEXT

CORRECTED TEXT

3 (1) APPLICANTS: Boon, Thierry, Van den
50 (2) INFORMATION FOR SEQUENCE ID NO: 1:
72 (2) INFORMATION FOR SEQUENCE ID NO: 2:
140 (2) INFORMATION FOR SEQUENCE ID NO: 3:
159 (2) INFORMATION FOR SEQUENCE ID NO: 4:
206 (2) INFORMATION FOR SEQUENCE ID NO: 5:
318 (2) INFORMATION FOR SEQUENCE ID NO: 6:
339 (2) INFORMATION FOR SEQUENCE ID NO: 7:
401 (2) INFORMATION FOR SEQUENCE ID NO: 8:
536 (2) INFORMATION FOR SEQUENCE ID NO: 9:
642 (2) INFORMATION FOR SEQUENCE ID NO: 10:
678 (2) INFORMATION FOR SEQUENCE ID NO: 11:
733 (2) INFORMATION FOR SEQUENCE ID NO: 12:
771 (2) INFORMATION FOR SEQUENCE ID NO: 13:
810 (2) INFORMATION FOR SEQUENCE ID NO: 14:
829 (2) INFORMATION FOR SEQUENCE ID NO: 15:
853 (2) INFORMATION FOR SEQUENCE ID NO: 16:

(1) APPLICANT: Boon, Thierry, Van den E
(2) INFORMATION FOR SEQ ID NO: 1:
(2) INFORMATION FOR SEQ ID NO: 2:
(2) INFORMATION FOR SEQ ID NO: 3:
(2) INFORMATION FOR SEQ ID NO: 4:
(2) INFORMATION FOR SEQ ID NO: 5:
(2) INFORMATION FOR SEQ ID NO: 6:
(2) INFORMATION FOR SEQ ID NO: 7:
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(2) INFORMATION FOR SEQ ID NO: 10:
(2) INFORMATION FOR SEQ ID NO: 11:
(2) INFORMATION FOR SEQ ID NO: 12:
(2) INFORMATION FOR SEQ ID NO: 13:
(2) INFORMATION FOR SEQ ID NO: 14:
(2) INFORMATION FOR SEQ ID NO: 15:
(2) INFORMATION FOR SEQ ID NO: 16: